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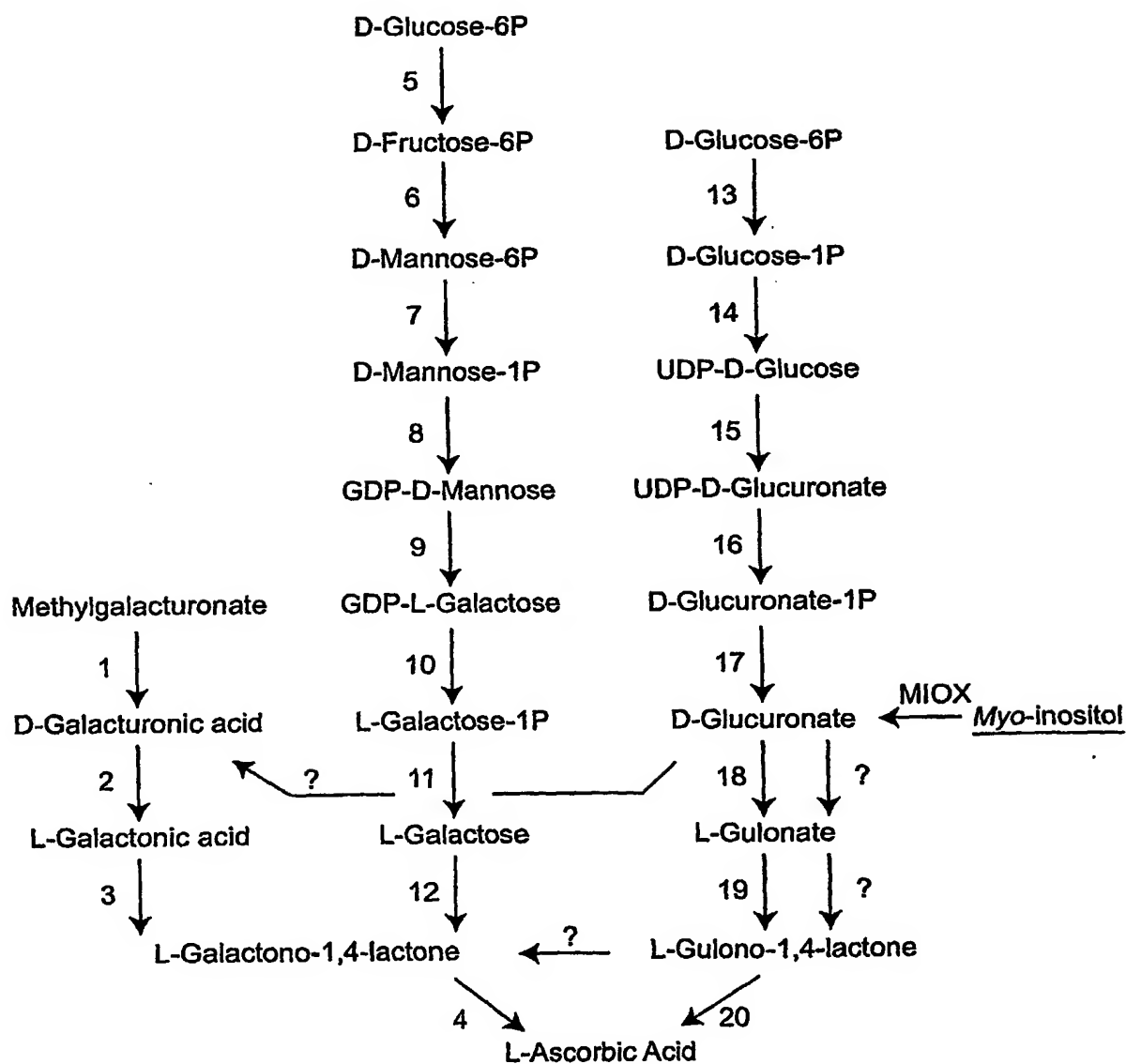
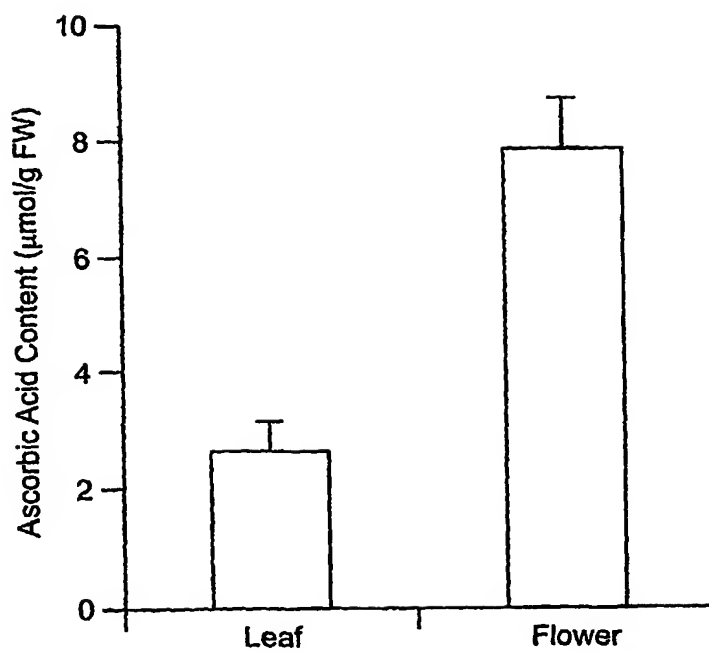
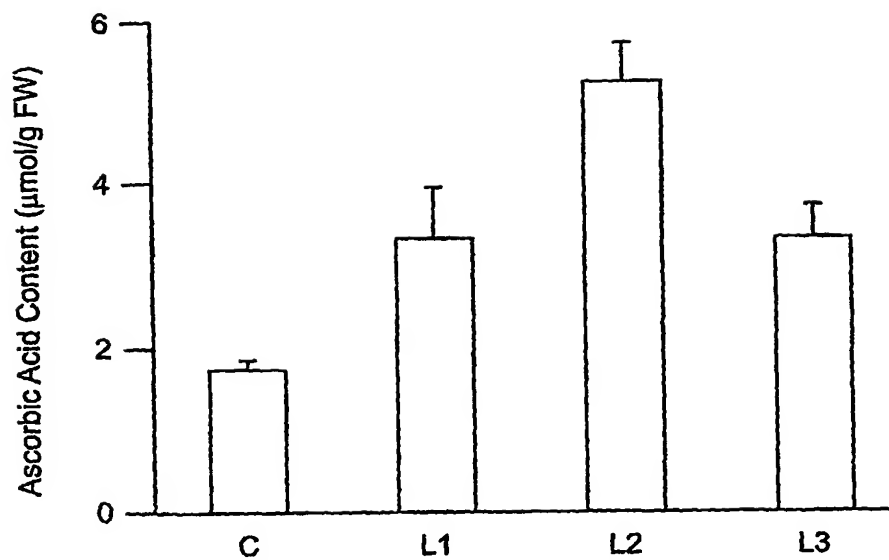
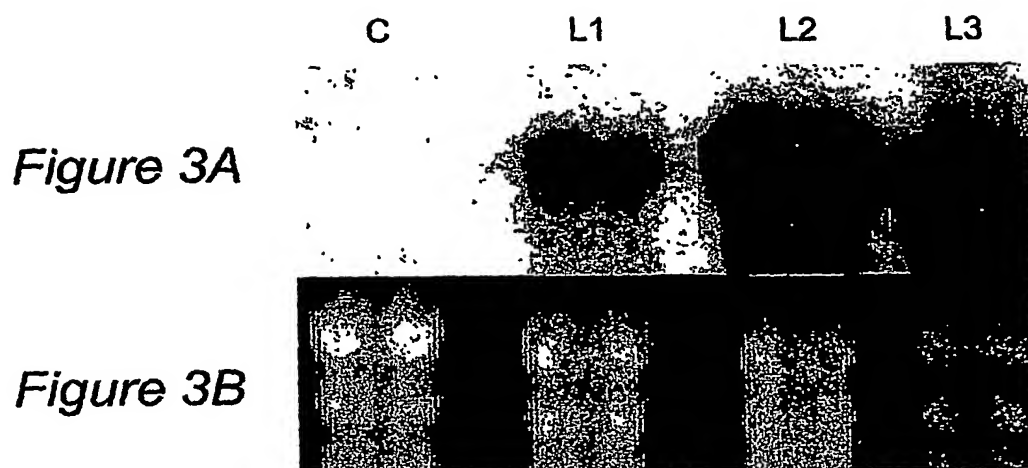


Figure 1

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*Figure 2A**Figure 2B**Figure 2C*

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*Figure 3C*

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SEQ ID NO:3

1	ATGACGATCT	CTGTTGAGAA	GCCGATTTTT	GAAGAAGAGG	TTTCTGCATT
51	CGAGAAGAGT	GGGGACAATA	TCGGAGAGTT	GAAATTGGAC	GGAGGATTTT
101	CGATGCCGAA	AATGGACACC	AATGACGACG	AAGCTTTTTT	GGCTCCTGAG
151	ATGAATGCAT	TTGGCCGCCA	ATTCAGGGAC	TACGATGTTG	ACAGTGAGAG
201	GCAAAAGGGC	GTCGAAGAGT	TTTACAGATT	ACGACACATC	AACCAAAC TG
251	TCGACTTTGT	GAAAAAGATG	AGGGCTGAAT	ATGGAAAATT	AGATAAAATG
301	GTGATGAGCA	TTTGGAATG	TTGTGAGCTT	CTCAATGAGG	TTGTCGATGA
351	GAGTGATCCA	GATCTTGACG	AGCCCCAGAT	TCAGCATTTG	CTTCAATCTG
401	CCGAAGCCAT	CCGCAAAGAT	TACCCTAATG	AAGATTGGCT	TCATCTGACC
451	GCTCTTATCC	ATGATCTTGG	GAAAGTTATT	ACTCTTCCAC	AATTCGGAGG
501	ACTTCCTCAA	TGGGCTGTTG	TTGGTGACAC	ATTCCCTGTT	GGATGTGCAT
551	TTGATGAATC	TAACGTACAT	CACAAGTACT	TTGTGGAAAA	CCCAGATTTT
601	CACAACGAAA	CCTACAACAC	TAAAAATGGG	ATTTACTCTG	AAGGGTGTGG
651	ATTAAACAAT	GTCATGATGT	CTTGGGGCCA	TGACGACTAC	ATGTACCTGG
701	TGGCTAAAGA	AAACGGAAGT	ACCTTGCCGT	CGGCTGGACA	GTTTATCATA
751	AGATACTACT	CCTTTTACCC	TTTGCACACG	GCTGGAGAAT	ACACCCATCT
801	TATGAACGAG	GAAGACAAGG	AGAATCTGAA	CTGGCTACAC	GTTTTCAACA
851	AGTACGACTT	GTACAGTAAG	AGCAAAGTTC	ACGTTGATGT	GGAGAAGGTC
901	GAGCCTTACT	ACATGTCTCT	TATCAAGAAA	TATTTCCCGG	AAAAC TTGAG
951	GTGG				

*Figure 4*

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SEQ ID NO:4

1	MTISVEKPIF	EEEVSAFEKS	GDNIGELKLD	GGFSMPKMDT	40
41	NDDEAFLAPE	MNAFGRQFRD	YDVESERQKG	VEEFYRLRHI	80
81	NQTVDFVKKM	RAEYGKLDKM	VMSIWECCCEL	LNEVVDESDP	120
121	DLDEPQIQHL	LQSAEAIRKD	YPNEDWLHLT	ALIHDLGKVI	160
161	TLPQFGGLPQ	WAVVGDTFPV	GCAFDESNVH	HKYFVENPDF	200
201	HNETYNTKNG	IYSEGCGLNN	VMMSWGHDDY	MYLVAKENG	240
241	TLPSAGQFII	RYHSFYPLHT	AGEYTHLMNE	EDKENLKWLH	280
281	VFNKYDLYSK	SKVHVDVEKV	EPYYMSLIKK	YFPENLRW	318

*Figure 5*